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OM protein - protein search using sw model

Run on: January 16, 2003, 16:42:17, Search time 18 0714 seconds
(without alignments)
58.517 Million cell updates/sec

Title: us-09-856-070-23

Perfect score: 55

Sequence: 1 ELMRLQDYEE 11

Scoring table: RIGSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	581	2 145889	ezrin - bovine
2	55	100.0	586	1 A34400	ezrin [validated]
3	55	100.0	630	2 147177	hypothetical prote
4	52	94.5	586	1 B41129	ezrin - mouse
5	38	69.1	140	2 B84133	hypothetical prote
6	38	69.1	150	2 C97449	hypothetical trans
7	38	69.1	150	2 AF2677	transcription fact
8	37	67.3	111	2 112857	hypothetical prote
9	37	67.3	321	2 H82832	protein export mem
10	37	67.3	337	1 A70364	conserved hypotet
11	37	67.3	1058	2 S65460	apolipoprotein B -
12	36	65.5	253	2 B83344	conserved hypotet
13	36	65.5	284	2 B84700	probable adenylyt
14	36	65.5	304	2 C82754	conserved hypotet
15	36	65.5	451	2 S01042	conserved hypotet
16	36	65.5	2472	2 A35715	iodin alpha chain
17	36	65.5	2477	1 SJCHA	iodin alpha chain
18	35	63.6	66	2 B84093	spectrin alpha cha
19	35	63.6	152	2 746984	hypothetical prote
20	35	63.6	221	2 H97212	hypothetical prote
21	35	63.6	477	2 101828	probable phosphor
22	35	63.6	892	1 PAU7AA	hypothetical prote
23	35	63.6	964	2 B59404	alpha actinin 1
24	35	63.6	4574	2 S02520	plectin isoform p1
25	35	63.6	4684	2 A59404	plectin - human
26	35	63.6	4687	1 A39638	plectin - rat
27	34	61.8	105	1 B69333	conserved hypotet
28	34	61.8	250	2 B84212	hypothetical prote
29	34	61.8	327	2 747000	ethanolamine phosph

ALIGNMENTS

RESULT 1

145889

ezrin - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 14-Aug-1999

C:Accession: 145889

R:Berenson, C.M.; Zhao, H.; Sajjoh, K.; Duman, R.S.; Nustler, E.J.

Mol. Cell. Neurosci. 4, 64-73, 1993

A>Title: Ezrin and osteonectin, two proteins associated with cell shape and growth, a

A:Reference number: 145889

A:Accession: 145889

A:Status: preliminary; translated from GK/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-581 <H6K>

A:Cross-references: GB:M08498; NID:q289407; FID:AAA0510.1; FID:q289408

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

F17-291/domain: protein 4.1 membrane-binding domain homology <B41>

Query Match 100.0%, Score 55, EA 2, Length 581;

Best local Similarity 100.0%; Pred. No. 0.017;

Matches 11, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 ELMRLQDYEE 11

DB 346 ELMRLQDYEE 356

RESULT 2

A34400

ezrin [validated] - human

R:Alternate names: cytovillin, p81 protein, villin 2

C:Species: Homo sapiens (man)

C>Date: 22 Jan 1990 #sequence_revision 14 Jul 1994 #text_change 08 Dec 2000

C:Accession: A34400; S04263; E61002

R:Turner, G.; Mizoguchi, R.; Fakkas, R.; Grieselink, K.H.; Wahlstrom, T.; Vaheri, A.

J. Biol. Chem. 264, 16727-16732, 1989

A>Title: Cytovillin, a microvillal Mem 75,000 protein, cDNA sequence, prokaryotic exp

A:Reference number: A34400; M010.85180259; FID:2674140

A:Accession: A34400

A:Molecule type: mRNA

A:Residues: 1-586 <TGR>

A:Cross-references: GB:05921

A>Note: the translation of residues 1-11 is not given

A>Note: parts of this sequence were confirmed by protein sequencing

R:Gould, K.L.; Bretschneider, A.; Esch, F.S.; Hunter, T.

EMBO J. 8, 4133-4142, 1989

A>Title: cDNA cloning and sequencing of the protein tyrosine kinase substrate, ezrin,

A:Reference number: S09263; M010.90076135; FID:2591371

A:Accession: S09263

A:Molecule type: mRNA

A:Residues: 2-580 <GGG>

A:Cross-references: GB:A51531; NID:q31282; FID:CAA35893.1; FID:q41283

K.Bauw, G.; Rasmussen, H.H.; Van den Hulster, M.; Van Damme, J.; Puyfer, M.; Gesser, B.; G. Electrophoresis 11: 528-536, 1990

A:Title: Two-dimensional gel electrophoresis, protein electrophoresis and microsequencing

A:Reference number: A61002; PMID:91031404; PMID:169755

A:Accession: E61002

A:Molecule type: protein

A:Residues: 255-263; 194, 196, 199, 201, 204, 270 <BAU>

A:Note: It is not certain whether this material represents ezrin or radixin (see entry A61001). This material corresponds to transformed epithelial amnion cell (AMA) database B61001. This protein is located in microvilli and is proposed to play a role in modulation of cell growth.

A:Gene: GH:VII.2

A:Cross-references: GH:120489; GIM:123900

A:Map position: 6q25-6q26

A:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton; membrane-associated protein; phosphoprotein

F:2-586/Product: ezrin; status: experimental <MA>

F:7-291/Domain: protein 4.1 membrane-binding domain homology <H1>

F:553-586/Region: actin binding; status: predicted

F:66/Binding site: phosphate (Ser) (covalent) #status: predicted

F:214,299,332/Binding site: phosphate (Thr) (covalent) #status: predicted

Query Match 100.0%; Score 55; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
IIIIIIIIII

Db 446 ELMRLQDYEE 456

RESULT 3

T47177
hypothetical protein DKFZp762H157.1 human (treatment)

C:Species: Homo sapiens (man)

C:Date: 20-Apr-2000 #sequence_revision 20 Apr 2000 #text_change 92-Sep-2000

C:Accession: T47177

Submitted to the Protein Sequence Database, March 2000

A:Reference number: 224377

A:Accession: T47177

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-640 <AAA>

A:Cross-references: EMBL:AL162086

A:Experimental source: adult melanoma (MeWo cell line); clone DKFZp762H157

C:Genetics:

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

Query Match 100.0%; Score 55; DB 2; Length 640
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
IIIIIIIIII

Db 490 ELMRLQDYEE 400

RESULT 4

T47129
ezrin - mouse

N:Alternate names: cytoவில்ლი; F-43 protein; radixin; villin 2

C:Species: Mus musculus (house mouse)

C:Date: 04-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999

C:Accession: T47129; EMBL:U01001; EMBL:U01001; EMBL:U01001

C:Pinayama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.

J. Cell Biol. 115: 1039-1048, 1991

A:Title: Radixin is a novel member of the band 4.1 family.

A:Reference number: A41129; PMID:92064635; PMID:1955455

A:Accession: T47129

A:Molecule type: mRNA

A:Residues: 1-586 <PUN>

A:Cross-references: EMBL:X66671; NID:q50880; PDB:CAA43086.1; PDB:q50881
R:Epstein, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Hirsch, A.; Samelson, L.E.
J. Immunol. 149: 1847-1852, 1992

A:Title: Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein in T cell

A:Reference number: A46501; PMID:92388649; PMID:1381389

A:Accession: C46501

A:Status: preliminary

A:Molecule type: protein

A:Residues: 412-426 <EG>

A:Experimental source: MRL lpr/lpr, T-cells

A:Note: sequence extracted from NCBI backbone (NCBI:112948)

A:Accession: A46501

A:Status: preliminary

A:Molecule type: protein

A:Residues: 27-33; 150, 152, 155 <EG>

A:Experimental source: MRL lpr/lpr, T-cells

A:Note: sequence extracted from NCBI backbone (NCBI:112948)

A:Accession: H46501

A:Status: preliminary

A:Molecule type: protein

A:Residues: 53-57, 148, 150, 152, 155 <EG>

A:Experimental source: MRL lpr/lpr, T-cells

A:Note: sequence extracted from NCBI backbone (NCBI:112940)

C:Comment: This protein is located in microvilli and is proposed to play a role in modulation of cell growth.

C:Keywords: actin binding; cytoskeleton; cytosol; membrane-associated protein; phosphoprotein

F:2-586/Product: ezrin; status: predicted <MA>

F:7-291/Domain: protein 4.1 membrane-binding domain homology <H1>

F:553-586/Region: actin binding; status: predicted

F:66/Binding site: phosphate (Ser) (covalent) #status: predicted

F:214,299,332/Binding site: phosphate (Thr) (covalent) #status: predicted

Query Match 94.5%; Score 52; DB 1; Length 586;
Best Local Similarity 90.9%; Pred. No. 0.065;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
IIIIIIIIII

Db 346 ELMRLQDYEE 356

RESULT 5

H84133
hypothetical protein H83872 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: H84133

K:Kakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H. Nucleic Acids Res. 28: 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A:Reference number: A46501; PMID:1058142

A:Accession: H84133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <STO>

A:Cross-references: GH:AP001520; GH:BA000004; NID:g10176401; PDB:HA0759.1; GSPPH:G

A:Experimental source: strain C-125

C:Genetics:

A:Gene: H83872

Query Match 69.1%; Score 48; DB 2; Length 140;
Best Local Similarity 87.5%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LRLQDYEE 11
IIIIIIIIII

Db 78 LRLQDYEE 85

RESULT 6

C97449
hypothetical transcription regulator y4td [imported] - Agrobacterium tumefaciens (str)

C:Species: Agrobacterium tumefaciens

[illegible]

Best Local Similarity 63.6%; Score 47; DB 1; Length 337;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMLRLQDYEE 11
DB 91 ELMLRLQDYAE 101

RESULT 10
A70464
conserved hypothetical protein aq_729 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A70464
C:Bankert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
V.
Nature 392, 454-458, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70464; MIM:681666; PMID:9537420
A:Accession: A70464
A:Status: preliminary; nucleic acid sequence not shown, translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <ACF>
A:Cross-references: GR:AF000705; GR:AE000557; NID:q2983310; PIDN:AA05914.1; PID:q298332
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_729
C:Superfamily: conserved hypothetical protein MJ0674

Query Match 67.3%; Score 47; DB 1; Length 337;
Best Local Similarity 77.8%; Score 47; DB 1; Length 337;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMLRLQDY 9
DB 150 EVMLELQDY 158

RESULT 11
S65460
apolipoprotein B - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 13-Aug-1999
C:Accession: S65460; I51362
C:Bank, P.J.; Deryckere, P.; Gannon, P.
Eur. J. Biochem. 230, 45-51, 1995
A:Title: Presence of an extended duplication in the putative low-density-lipoprotein re
A:Reference number: I51362; MIM:542454; PMID:7541349
A:Accession: S65460
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1058 <BAF>
A:Cross-references: EMBL:X81856; NID:q854519; PIDN:CAAS7444.1; PID:q854520
A:Experimental source: liver
C:Genetics:
A:Gene: apob
C:Superfamily: apolipoprotein B
C:Keywords: calcium; cholesterol metabolism; glycoprotein; intestine; LDL;

Query Match 67.3%; Score 47; DB 2; Length 1058;
Best Local Similarity 63.6%; Score 47; DB 2; Length 1058;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELMLRLQDYEE 11
DB 1014 ETOLKLHWEE 1024

RESULT 12
A83244
conserved hypothetical protein PA3198 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83244
R:Stover, C.K.; Plam, X.Q.; Erwin, A.L.; Maseduchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.K.; Kas, A.; Jarboe, K.L.;
Lory, S.; Olson, M.V.
Nature 406, 954-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MIM:20437337; PMID:10984043
A:Accession: A83244
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <SIO>
A:Cross-references: GB:AE004744; GB:AE004091; NID:q9949417; PIDN:AA06586.1; GSPUB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3198

Query Match 65.5%; Score 46; DB 2; Length 250;
Best Local Similarity 70.0%; Score 46; DB 2; Length 250;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMLRLQDYEE 10
DB 88 ELMLRLQDYEE 97

RESULT 13
D84790
probable adenylate kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 03-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84790
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Renito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Gront, L.A.; Shen, M.; VanAken, S.E.; Unayama, T.; Tallon,
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventor
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MIM:20083487; PMID:10617147
A:Accession: D84790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-284 <STG>
A:Cross-references: GB:AF002054; NID:q4056480; PIDN:AA098046.1; GSPUB:GN00139
C:Genetics:
A:Gene: At2g37250
A:Map position: 2

Query Match 65.5%; Score 46; DB 2; Length 284;
Best Local Similarity 87.5%; Score 46; DB 2; Length 284;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ELMLRLQDYEE 11
DB 271 ELMLRLQDYEE 278

RESULT 14
G82554
conserved hypothetical protein XE2451 [imported] - Xylella fastidiosa (strain 9a%)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: G82554
C:Anonymous, The Xylella fastidiosa Consortium of the organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MIM:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <SLM>
A:Cross-references: GR:AF004054; GR:AE003849; NID:q9107645; PIDN:AA085250.1; GSPUB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Arcencio, M.; Alvares, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer, H.
 as-Neto, E.; Docena, C.; El-Dodry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Furo, J.A.; Piaga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Komor, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.Y.
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, P.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.F.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Ishikawa, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski Almeida, S.; Vettore, A.L.;
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XP2451

Query Match 65.5%; Score 36; DB 2; Length 338;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYE 10
 ||| |||:
 DB 171 ELVRLQDYE 180

RESULT 15

S01092

fodrin alpha chain (clone alpha-2) - African clawed frog (fragment)

N:Alternate names: nonerythroid spectrin alpha chain

C:Species: Xenopus laevis (African clawed frog)

C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 20-Jun-2000

C:Accession: S01092

R:Gibbelhaus, D.H.; Zelus, B.D.; Henchman, S.K.; Moon, R.T.

J. Cell Biol. 105, 843-853, 1987

A:Title: Changes in the expression of alpha-fodrin during embryonic development of xenop

A:Reference number: S01091; MRP-87368388; PMID:3040772

A:Accession: S01092

A:Molecule type: mRNA

A:Residues: 1-454 <GIF>

A:Cross-references: EMBL:X06042; NID:964700; PIDN:CAA29435.1; PID:gl334648

C:Superfamily: spectrin alpha chain, calmodulin repeat homology; SH3 homology; spectrin/

C:Keywords: actin binding; EF hand

E:5 109/Domain: spectrin/dystrophin repeat homology <SP6>

E:110-225/Domain: spectrin/4.1G-phi repeat homology <SF7>

E:216-321/Domain: spectrin/dystrophin repeat homology <SH8>

E:407-454/Domain: SH3 homology <SH3>

Query Match 65.5%; Score 36; DB 2; Length 454;

Best Local Similarity 63.6%; Pred. No. 54;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELMRLQDYE 11
 ||| |||:
 DB 403 ELVRLQDYE 413

Search completed: January 16, 2003, 16:57:52

Job time : 19.0714 secs

